AMENDMENTS

IN THE CLAIMS

Please amend the claim set to read as follows:

1-3. (Canceled)

4. (Currently amended) A method for analyzing a sequence of a template, said method comprising:
   (a) capturing the template with a sequencing reagent to form a captured template, said sequencing reagent comprising:
      i. a capture moiety;
      ii. a spacer region; and
      iii. a primer region, wherein said primer region is adjacent to said spacer region **and said primer region comprises from 3-7 bases**;
   (b) forming a primer-polymerase complex, said primer-polymerase complex comprising said primer region and a polymerase;
   (c) scanning the captured template using said primer-polymerase complex for a region of complementarity to said primer region and forming a **transient** duplex, wherein said region of complementarity to said primer region is not adjacent to a region that is capable of forming a duplex with said spacer region;
   (d) extending the primer by at least one nucleotide moiety by means of a template-homology dependent extension reaction to form an extended primer; and
   (e) detecting said extended primer, wherein detecting said extended primer indicates the presence of one or more regions of complementarity to the primer in the captured template.

5. (Currently amended) The method of Claim 4 wherein the **sequencing** ~~sequence~~ reagent[s are] **is** immobilized to a solid surface.

6. (Original) The method of Claim 5 wherein the solid surface is glass or plastic.

7. (Original) The method of claim 5 wherein the solid surface is a glass plate, a quartz wafer, a nylon membrane, a nitrocellulose membrane, or a silicon wafer.

8. (Previously presented) The method of Claim 5 wherein the solid surface is silicon glass.

9. (Original) The method of Claim 5 wherein the solid surface is polystyrene plastic.

10. (Currently amended) The method of Claim 4 wherein the **sequencing** ~~sequence~~ reagent further comprises an attachment moiety.

11. (Currently amended) The method of Claim 10 wherein the attachment moiety is located at or near the 5'-terminus of the **sequencing** ~~sequence~~ reagent.

12. (Original) The method of Claim 10 wherein the attachment moiety is an amino group, a thiol group, a disulfide group, or a biotin group.

13. (Previously presented) The method of Claim 4, wherein the capture moiety is on a first reagent and the primer region is on a second reagent, and said first reagent and said second reagent are not attached to one another.

14. (Original) The method of Claim 13 wherein the first reagent is proximal to the second reagent on a solid phase.

15. (Original) The method of Claim 4 wherein the capture moiety comprises a sequence of 8-24 cytosine bases.

16. (Original) The method of Claim 4 wherein the capture moiety comprises a specific sequence complementary to a PCR primer or a portion thereof.

17. (Previously presented) The method of claim 4 wherein the spacer region is at least 10 nm in length.

18. (Original) The method of Claim 4 wherein the spacer region comprises a random, pseudo-random, or non-random sequence of nucleotide bases or analogs thereto.

19. (Previously presented) The method of Claim 4, wherein the at least one nucleotide moiety is a non-chain terminating nucleotide or an analog of a non-chain terminating nucleotide

20. (Previously presented) The method of Claim 19, wherein the at least one nucleotide moiety is a deoxynucleoside triphosphate base or a ribonucleoside triphosphate base.

21. (Canceled)

22. (Canceled)

23. (Currently amended) The method of Claim 4, wherein at least one nucleotide moiety [is detectably labeled] **has a detectable label**.

24. (Original) The method of Claim 23 wherein the detectable label is a fluorescent label.

25. (Original) The method of Claim 23 wherein the detectable label is a radioactive isotope.

26. (Original) The method of Claim 23 wherein the detectable label is an electron rich molecule.

27. (Previously presented) The method of Claim 4, wherein the extended primer is detected by change in mass.

28. (Currently amended) The method of Claim 4 **further comprising using a plurality of said sequencing reagents on an array,** wherein the density of **said plurality of said sequencing** ~~sequence~~ reagents in the array is at least 1000 elements/cm^2.

29. (Withdrawn) A sequence array comprising one or more sequence reagents in an orderly arrangement wherein each reagent comprises:
    (i) a capture moiety which can form a stable complex with a region of a template nucleic acid molecule;
    (ii) a spacer region; and
    (iii) a primer region, wherein said primer region comprises 3-7 bases.

30. (Withdrawn) The sequence array of Claim 29 wherein the array comprises a set, subset, or combination of 4^3 - 4^7 different sequence reagents.

31. (Canceled)

32. (Canceled)

33. (Previously presented) The method according to Claim 4, wherein said primer consists of from 4 to 6 bases.

34. (Previously presented) The method according to claim 4, wherein said spacer is between said capture moiety and said primer region.

35. (Previously presented) The method of Claim 4, wherein the method is performed using a plurality of sequencing reagents, and said plurality of sequencing reagents are used to form a plurality of primer-polymerase complexes on an array.

36. (Previously presented) The method of Claim 4, wherein the spacer is comprised of at least one substance selected from the group consisting of a PNA sequence, polyethylene glycol groups, and 5-nitroindole groups.